



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/208,629G  
Source: 1600  
Date Processed by STIC: 3/17/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

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**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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**Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:**

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



1600

## RAW SEQUENCE LISTING

DATE: 03/17/2004

PATENT APPLICATION: US/09/208,629G

TIME: 15:54:21

Input Set : A:\22000-20603.10.txt

Output Set: N:\CRF4\03172004\I208629G.raw

4 <110> APPLICANT: COUGHLIN, Shaun R.  
5 ISHIHARA, Hiroaki  
6 CONNOLLY, Andrew  
8 <120> TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR 3 AND USES  
9 THEREOF  
11 <130> FILE REFERENCE: 220002060310  
13 <140> CURRENT APPLICATION NUMBER: US 09/208,629G  
14 <141> CURRENT FILING DATE: 1998-12-08  
16 <150> PRIOR APPLICATION NUMBER: US 08/742,440  
17 <151> PRIOR FILING DATE: 1996-10-30  
19 <160> NUMBER OF SEQ ID NOS: 25  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1224  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Mus Musculus  
28 <400> SEQUENCE: 1  
29 tgactttgta tacttaacaa catcctgtag ccgggtctca ggacatcaag atgaaaatcc 60  
30 ttatcttggt tgcagctggg ctgctgttct tgccagtcac tgtttgccaa agtggcataa 120  
31 atgtttcaga caactcagca aagccaacct taactattaa gagttttaat ggggggtcccc 180  
32 aaaatacctt tgaagaattc ccactttctg acatagaggg ctggacagga gccaccacaa 240  
33 ctataaaagc ggagtgtccc gaggacagta tttcaactct ccacgtgaat aatgctacca 300  
34 taggatacct gagaagttcc ttaagtaccc aagtgtatcc tgccatctat atcctgtctgt 360  
35 ttgtggttgg tgtaccatcc aacatcgtga ccctgtggaa actctcctta aggaccaa 420  
36 ccatcagctc ggtcatcttt cacaccaacc tggccatcgc agatctcctt ttctgtgtca 480  
37 cactgccatt taagatcgcc taccatctca atggcaacaa ctgggtattt ggcgagggtca 540  
38 tgtgccggat caccacgggc gttttctacg gcaacatgta ctgcgctatc ctgatcctca 600  
39 cttgcatggg catcaaccgc tacctggcca cggctcacc tttcacatac cagaagctgc 660  
40 ccaaacgcag cttctccttg ctcatgtgtg gcatagtgtg ggtcatggtt ttcttatata 720  
41 tgcctgccct tgcctcctg aagcaggagt accacctcgt ccactcagag atcaccacct 780  
42 gccacgatgt cgtcgacggc tgcgagtcct catcatcctt ccgattctac tacttgcgtc 840  
43 ccttagcatt ctttgggttc ctcatcccg tttgtgatcat catcttctgt tacacgactc 900  
44 tcatccacaa acttaaatca aaggatcgga tatggctggg ctacatcaag gccgtcctcc 960  
45 tcatccttgt gattttcaca atttgctttg cccccacaa catcactact gtaatccacc 1020  
46 atgccaaact ctactaccac aataccgaca gcttgactt tatgtatctt attgctctgt 1080  
47 gcctggggag cctgaatagc tgcctagatc cattccttta ctttgtcatg tcgaaagttg 1140  
48 tagatcagct taatccttag tcggcaatgg caagaccact ttagagacca aggagagata 1200  
49 tctgggaaga catacatgct tggc 1224  
51 <210> SEQ ID NO: 2  
52 <211> LENGTH: 1124  
53 <212> TYPE: DNA  
54 <213> ORGANISM: Mus Musculus  
56 <220> FEATURE:

## RAW SEQUENCE LISTING

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*"C" is at 22*

Input Set : A:\22000-20603.10.txt

Output Set: N:\CRF4\03172004\I208629G.raw

*"a" is at 27*

57 <221> NAME/KEY: misc feature  
 58 <222> LOCATION: 22, 27, 117, 118, 119, 120, 121, 122, 123, 350, 351, 442,  
 59 443, 444, 595, 596, 597, 663, 785, 859, 860, 861, 862, 863,  
 60 864

61 &lt;223&gt; OTHER INFORMATION: n = A, T, C, or G

63 &lt;400&gt; SEQUENCE: 2

W--> 64 ccatatgcta atatttcctt tcaattacag gcataaatgt ttcagacaac tcagcaaagc 60  
 65 caaccttaac tattaagagt tttaatgggg gtccccaataa tacctttgaa gaattcnnnn 120  
 66 nnntacaact ctccatgtga ataatgctac catgggatac ctgagaagtt ccttaagtac 180  
 67 caaagtata cctgccatct acatcctggg gtttgtgatt ggtgtaccag cgaacatcgt 240  
 68 gacctgtgg aaactctcct caaggaccaa atccatctgt ctggtcatct ttcacaccaa 300  
 69 cctggccatc gcggatctcc tttctgtgtg cacgtgccc ttttaagatc ncctaccatc 360  
 70 tcaatggcaa caactgggta tttggcgagg tcatgtgccg gatcaccacg gtcgttttct 420  
 71 acggcaacat gtactgcgct annntcctga tcctcacctg catgggcac caccgctacc 480  
 72 tggccacggc tcaccctttc acataaccaga agctgcccaa acgcagcttc tccatgctca 540  
 73 tgtgtggcat ggtgtgggtc atggttttct tatacatgct gccctttgtc atccnnnaag 600  
 74 caggagtacc acctcgtcca ctccgagatc accacctgcc acgatgtcgt cgacgcgtgc 660  
 75 gantcccat catccttccg attctactac ttcgtctcct tagcattctt tgggttcctc 720  
 76 atcccgtttg tgatcatcat cttctgttac acgactctca tccacaaact taaatcaaaa 780  
 77 gatcngatat ggctgggcta catcaaggcc gtctcctca tccttgtgaa tttcaccatc 840  
 78 tgcttccccc ccaccaagnn nnnngatata tgggaagacg tacatgcttg gctgacttgt 900  
 79 gcatggcacc atcagctcaa tttttaattt ttttaattta atttaattta attttatgtt 960  
 80 tttgagacag agcctcactg tgtagtctct gctggcctgg ctggttctct atttagacca 1020  
 81 ggtagcctt gaactcacag agatctgcct gcttctgcct cccaagtgtt gggttcaacc 1080  
 82 aggtctggca agcgtccat ttttcagctc ctctgcaaca gtgc 1124

84 &lt;210&gt; SEQ ID NO: 3

85 &lt;211&gt; LENGTH: 369

86 &lt;212&gt; TYPE: PRT

87 &lt;213&gt; ORGANISM: Mus Musculus

89 &lt;400&gt; SEQUENCE: 3

90 Met Lys Ile Leu Ile Leu Val Ala Ala Gly Leu Leu Phe Leu Pro Val  
 91 1 5 10 15  
 92 Thr Val Cys Gln Ser Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro  
 93 20 25 30  
 94 Thr Leu Thr Ile Lys Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu  
 95 35 40 45  
 96 Glu Phe Pro Leu Ser Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr  
 97 50 55 60  
 98 Ile Lys Ala Glu Cys Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn  
 99 65 70 75 80  
 100 Asn Ala Thr Ile Gly Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile  
 101 85 90 95  
 102 Pro Ala Ile Tyr Ile Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile  
 103 100 105 110  
 104 Val Thr Leu Trp Lys Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val  
 105 115 120 125  
 106 Ile Phe His Thr Asn Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr  
 107 130 135 140  
 108 Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe

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109 145          150          155          160
110 Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met
111          165          170          175
112 Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu
113          180          185          190
114 Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe
115          195          200          205
116 Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met
117          210          215          220
118 Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu
119 225          230          235          240
120 Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser
121          245          250          255
122 Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile
123          260          265          270
124 Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu
125          275          280          285
126 Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu
127          290          295          300
128 Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Thr Asn Ile Ile Leu
129 305          310          315          320
130 Val Ile His His Ala Asn Tyr Tyr Tyr His Asn Thr Asp Ser Leu Tyr
131          325          330          335
132 Phe Met Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys Leu
133          340          345          350
134 Asp Pro Phe Leu Tyr Phe Val Met Ser Lys Val Val Asp Gln Leu Asn
135          355          360          365
136 Pro

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140 &lt;210&gt; SEQ ID NO: 4

141 &lt;211&gt; LENGTH: 1224

142 &lt;212&gt; TYPE: DNA

143 &lt;213&gt; ORGANISM: Homo Sapiens

145 &lt;400&gt; SEQUENCE: 4

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146 tgctccatga ttttacagat ttcataacgt ttaagagacg ggactcaggt catcaaaatg 60
147 aaagccctca tctttgcagc tgcctggcctc ctgcttctgt tgcccacttt ttgtcagagt 120
148 ggcattggaaa atgatacaaa caacttggca aagccaacct taccatttaa gacctttcgt 180
149 ggagctcccc caaattcttt tgaagagttc cccttttctg ccttgggaagg ctggacagga 240
150 gccacgatta ctgtaaaaat taagtgcctt gaagaaagtg cttcacatct ccatgtgaaa 300
151 aatgctacca tgggttacct gaccagctcc ttaagtacta aactgatacc tgccatctac 360
152 ctctctggtg ttgtagttgg tgtcccggcc aatgctgtga cctgtggat gcttttcttc 420
153 aggaccagat ccatctgtac cactgtattc tacaccaacc tggccattgc agattttctt 480
154 ttttgtgtta cattgccctt taagatagct tatcatctca atgggaacaa ctgggtattt 540
155 ggagaggtcc tgtgcggggc caccacagtc atcttctatg gcaacatgta ctgctccatt 600
156 ctgctccttg cctgcatcag catcaaccgc taccctggca tcgtccatcc tttcacctac 660
157 cggggcctgc ccaagcacac ctatgccttg gtaacatgtg gactggtgtg ggcaacagtt 720
158 ttcttatata tgcctgccatt tttcatactg aagcaggaat attatcttgt tcagccagac 780
159 atcaccacct gccatgatgt tcacaacact tgcgagtcct catctccctt ccaactctat 840
160 tacttcatct ccttggcatt ctttggattc ttaattccat ttgtgcttat catctactgc 900
161 tatgcagcca tcatccggac acttaatgca tacgatcata gatggttgtg gtatgttaag 960

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Output Set: N:\CRF4\03172004\I208629G.raw

162 gcgagtctcc tcctccttgt gattttttacc atttgctttg ctccaagcaa tattattctt 1020  
 163 attattcacc atgctaacta ctactacaac aacactgatg gcttatattt tatatatctc 1080  
 164 atagctttgt gcctgggtag tcttaatagt tgcttagatc cattccttta ttttctcatg 1140  
 165 tcaaaaacca gaaatcactc cactgcttac cttacaaaat agtgaaatga tcttagagaa 1200  
 166 caaggacagc catcacagag aacg 1224

168 &lt;210&gt; SEQ ID NO: 5

169 &lt;211&gt; LENGTH: 1102

170 &lt;212&gt; TYPE: DNA

171 &lt;213&gt; ORGANISM: Homo Sapiens

173 &lt;400&gt; SEQUENCE: 5

174 acaggcatgg aaaatgatac aaacaacttg gcaaagccaa ccttaccat taagaccttt 60  
 175 cgtggagctc ccccaaattc ttttgaagag ttcccctttt ctgccttgga aggctggaca 120  
 176 ggagccacga ttactgtaaa aattaagtgc cctgaagaaa gtgcttcaca tctccatgtg 180  
 177 aaaaatgcta ccatggggta cctgaccagc tccttaagta ctaaactgat acctgccatc 240  
 178 tacctcctgg tgttttagt tgggtgtccc gccaatgctg tgaccctgtg gatgcttttc 300  
 179 ttcaggacca gatccatctg taccactgta ttctacacca acctggccat tgcagatttt 360  
 180 cttttttgtg ttacattgcc ctttaagata gcttatcatc tcaatgggaa caactgggta 420  
 181 tttggagagg tctgtgccc ggccaccaca gtcatcttct atggcaacat gtactgtccc 480  
 182 attctgtctc ttgcctgcat cagcatcaac cgctacctgg ccatcgtcca tcctttcacc 540  
 183 taccggggcc tgcccaagca cacctatgcc ttggtaacat gtggactggt gtgggcaaca 600  
 184 gttttcttat atatgctgcc atttttcata ctgaagcagg aatattatct tgttcagcca 660  
 185 gacatcacca cctgccatga tgttcacaac acttgcgagt cctcatctcc cttccaactc 720  
 186 tattacttca tctccttggc attccttggga ttcttaattc catttgtgct tatcatctac 780  
 187 tgctatgcag ccatcatccg gacacttaat gcatacgatc atagatgggt gtggtatggt 840  
 188 aaggcgagtc tctcatcct tgtgattttt accatttgc tttgctccaag caatattatt 900  
 189 cttattattc accatgctaa ctactactac aacaacactg atggcttata ttttatatat 960  
 190 ctcatagctt tggcctggg tagtcttaat agttgcttag atccattcct ttattttctc 1020  
 191 atgtcaaaaa ccagaaatca ctccactgct taccttacia aatagtgaat tgatcttaga 1080  
 192 gaacaaggac agccatcaca ga 1102

194 &lt;210&gt; SEQ ID NO: 6

195 &lt;211&gt; LENGTH: 374

196 &lt;212&gt; TYPE: PRT

197 &lt;213&gt; ORGANISM: Homo Sapiens

199 &lt;400&gt; SEQUENCE: 6

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 201 1 5 10 15  
 202 Thr Phe Cys Gln Ser Gly Met Glu Asn Asp Thr Asn Asn Leu Ala Lys  
 203 20 25 30  
 204 Pro Thr Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe  
 206 35 40 45  
 207 Glu Glu Phe Pro Phe Ser Ala Leu Glu Gly Trp Thr Gly Ala Thr Ile  
 208 50 55 60  
 209 Thr Val Lys Ile Lys Cys Pro Glu Glu Ser Ala Ser His Leu His Val  
 210 65 70 75 80  
 211 Lys Asn Ala Thr Met Gly Tyr Leu Thr Ser Ser Leu Ser Thr Lys Leu  
 212 85 90 95  
 213 Ile Pro Ala Ile Tyr Leu Leu Val Phe Val Val Gly Val Pro Ala Asn  
 214 100 105 110  
 215 Ala Val Thr Leu Trp Met Leu Phe Phe Arg Thr Arg Ser Ile Cys Thr

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```

216      115      120      125
217 Thr Val Phe Tyr Thr Asn Leu Ala Ile Ala Asp Phe Leu Phe Cys Val
218      130      135      140
219 Thr Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val
220 145      150      155      160
221 Phe Gly Glu Val Leu Cys Arg Ala Thr Thr Val Ile Phe Tyr Gly Asn
222      165      170      175
223 Met Tyr Cys Ser Ile Leu Leu Leu Ala Cys Ile Ser Ile Asn Arg Tyr
224      180      185      190
225 Leu Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro Lys His Thr
226      195      200      205
227 Tyr Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val Phe Leu Tyr
228      210      215      220
229 Met Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu Val Gln Pro
230 225      230      235      240
231 Asp Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu Ser Ser Ser
232      245      250      255
233 Pro Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe Gly Phe Leu
234      260      265      270
235 Ile Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile Ile Arg Thr
236      275      280      285
237 Leu Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys Ala Ser Leu
238      290      295      300
239 Leu Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser Asn Ile Ile
240 305      310      315      320
241 Leu Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr Asp Gly Leu
242      325      330      335
243 Tyr Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu Asn Ser Cys
244      340      345      350
245 Leu Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg Asn His Ser
246      355      360      365
247 Thr Ala Tyr Leu Thr Lys
248      370
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 425
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo Sapiens
256 <400> SEQUENCE: 7
257 Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
258 1      5      10      15
259 Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
260      20      25      30
261 Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
262      35      40      45
263 Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
264      50      55      60
265 Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
266 65      70      75      80
267 Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu

```

**RAW SEQUENCE LISTING ERROR SUMMARY**  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 117,118,119,120,121,122,123,350,351,442,443,444,595,596,597

Seq#:2; N Pos. 663,785,859,860,861,862,863,864

Seq#:10; N Pos. 3,12,18,21,22,24,27

Seq#:11; N Pos. 6,9,12,15,21,24

Seq#:21; Xaa Pos. 1

Seq#:22; Xaa Pos. 1

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/208,629G

DATE: 03/17/2004

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Input Set : A:\22000-20603.10.txt

Output Set: N:\CRF4\03172004\I208629G.raw

L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60  
M:341 Repeated in SeqNo=2  
L:389 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:397 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:408 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:412 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:416 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:537 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21  
L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:556 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:560 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22  
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0